GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 24, 2003, 15:45:24 ; Search time 17.6061 Seconds
(without alignments)
628.181 Million cell updates/sec

Title: US-09-988-971-2_COPY_94_176
Perfect score: 446
Sequence: 1 WLYEGLSREKAEELLLLPGN.....WLYISPRLTFPSLQALVDHY 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	446	100.0	210	23	AAO15458	Mouse modulator of
2	446	100.0	261	23	AAO15457	Human modulator of
3	446	100.0	261	23	AAU91308	Human protein NOV1
4	443	99.3	248	21	AAB42993	Human ORFX ORF2757
5	412	92.4	259	23	AAO15456	Mouse modulator of
6	254	57.0	505	22	AAB99332	Human tyrosine kin
7	233	52.2	315	22	AAU31072	Novel human secret
8	228	51.1	101	18	AAW31184	Human p56-lck prot
9	228	51.1	134	17	AAW03982	DET1-DET2-spacer-e
10	228	51.1	134	17	AAW02120	DET1-DET2-spacer-e
11	228	51.1	134	18	AAW11286	DET1-DET2-spacer-e
12	228	51.1	134	18	AAW19624	Human lck SH2 doma
13	228	51.1	224	18	AAW14788	FKBP-LCK:SH2 fusio
14	228	51.1	224	20	AAW96823	A fusion protein o
15	228	51.1	508	21	AAB37700	Human lymphocyte k
16	228	51.1	509	21	AAY49420	PKA substrate, Src
17	222.5	49.9	102	16	AAR72090	Lck SH2 region. N
18	214	48.0	94	20	AAY29670	Human src-family k
19	214	48.0	94	22	AAU08732	Src-family kinase
20	214	48.0	496	20	AAY29668	Human src-family k
21	214	48.0	496	22	AAU08730	Xenopus laevis src
22	214	48.0	496	22	AAU08734	Xenopus laevis src
23	214	48.0	496	22	AAU08735	Xenopus laevis src
24	212	47.5	541	23	AAU74614	Perinuclear theca
25	212	47.5	543	20	AAY24421	Human yes1 protein
26	212	47.5	543	22	ABG10302	Novel human diagno
27	212	47.5	543	22	AAB84663	Amino acid sequenc
28	212	47.5	1046	22	ABG20772	Novel human diagno
29	211	47.3	417	12	AAR14201	(Beta-galactosidas
30	211	47.3	502	23	AAE21689	Fugu rubripes lymp
31	211	47.3	551	22	ABG22264	Novel human diagno.
32	206	46.2	117	17	AAW03986	SH2 domain from hu
33	206	46.2	117	17	AAW02124	Human fyn SH2 doma
34	198.5	44.5	517	22	ABB57957	Drosophila melanog
35	187	41.9	552	22	ABB57777	Drosophila melanog
36	187	41.9	552	22	ABB66713	Drosophila melanog
37	186	41.7	98	19	AAW59756	Amino acid sequenc
38	186	41.7	98	19	AAW59760	Amino acid sequenc
39	186	41.7	100	22	AAB19979	Rous sarcoma virus
40	186	41.7	251	21	AAY44450	Mutant chicken c-S
41	186	41.7	533	14	AAR39705	Chicken pp60 c-src
42	186	41.7	533	21	AAY44447	Wild-type chicken
43	186	41.7	533	21	AAY44449	Mutant chicken c-S
44	186	41.7	533	21	AAY44451	Mutant chicken c-S
45	186	41.7	533	22	AAB84661	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAO15458
ID AAO15458 standard; Protein; 210 AA.
XX
AC AAO15458;
XX
DT 03-OCT-2002 (first entry)
XX
DE Mouse modulator of antigen receptor signalling short isoform protein.
XX
KW Mouse; gene therapy; modulator of antigen receptor signalling; MARS;
KW tumour suppressor gene; Scr-like adaptor protein; SLAP;
KW myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder;
KW immunosuppression; myeloproliferative disorder; breast cancer.
XX
OS Mus sp.
XX
PN WO200242452-A2.
XX
PD 30-MAY-2002.
XX
PF 26-NOV-2001; 2001WO-CA01662.
XX
PR 27-NOV-2000; 2000CA-2324663.
XX
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
PI Mcglade JC, Loreto MP;
XX
DR WPI; 2002-566564/60.
DR N-PSDB; AAL44090.
XX
PT New isolated modulator of antigen receptor signaling protein or its

PT fragment, useful for treating malignant disorders such as myeloid
PT malignancies, autoimmune disorders and myeloproliferative disorders -
XX
PS Claim 8; Page 78; 110pp; English.
XX
CC The invention comprises the amino acid and coding sequences of modulator
CC of antigen receptor signalling (MARS) proteins. The MARS protein is a
CC putative tumour suppressor gene and exhibits structural and sequence
CC similarity to the Scr-like adaptor protein (SLAP). The MARS DNA and
CC protein sequences of the invention are useful for the treatment of
CC myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune
CC disorders, immunosuppression, myeloproliferative disorders and
CC malignancies related to the de-regulation of tyrosine kinases (e.g.
CC breast cancer). The present amino acid sequence represents a mouse MARS
CC protein.
XX
SQ Sequence 210 AA;

Query Match 100.0%; Score 446; DB 23; Length 210;
Best Local Similarity 100.0%; Pred. No. 3.9e-50;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 94 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 153

Qy 61 DNGWLYISPRLTFPSLQALVDHY 83
|||||||||||||||||||||||
Db 154 DNGWLYISPRLTFPSLQALVDHY 176

RESULT 2
AAO15457
ID AAO15457 standard; Protein; 261 AA.
XX
AC AAO15457;
XX
DT 03-OCT-2002 (first entry)
XX
DE Human modulator of antigen receptor signalling (MARS) protein.
XX
KW Human; gene therapy; modulator of antigen receptor signalling; MARS;
KW tumour suppressor gene; Scr-like adaptor protein; SLAP;
KW myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder;
KW immunosuppression; myeloproliferative disorder; breast cancer.
XX
OS Homo sapiens.
XX
PN WO200242452-A2.
XX
PD 30-MAY-2002.
XX
PF 26-NOV-2001; 2001WO-CA01662.
XX
PR 27-NOV-2000; 2000CA-2324663.
XX
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
PI Mcglade JC, Loreto MP;
XX
DR WPI; 2002-566564/60.
DR N-PSDB; AAL44089.
XX
PT New isolated modulator of antigen receptor signaling protein or its
PT fragment, useful for treating malignant disorders such as myeloid
PT malignancies, autoimmune disorders and myeloproliferative disorders -
XX
PS Claim 7; Fig 9A; 110pp; English.
XX
CC The invention comprises the amino acid and coding sequences of modulator
CC of antigen receptor signalling (MARS) proteins. The MARS protein is a
CC putative tumour suppressor gene and exhibits structural and sequence
CC similarity to the Scr-like adaptor protein (SLAP). The MARS DNA and
CC protein sequences of the invention are useful for the treatment of
CC myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune
CC disorders, immunosuppression, myeloproliferative disorders and
CC malignancies related to the de-regulation of tyrosine kinases (e.g.
CC breast cancer). The present amino acid sequence represents a human MARS
CC protein.
XX
SQ Sequence 261 AA;

Query Match 100.0%; Score 446; DB 23; Length 261;
Best Local Similarity 100.0%; Pred. No. 5.1e-50;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 94 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 153

Qy 61 DNGWLYISPRLTFPSLQALVDHY 83
|||||||||||||||||||||||
Db 154 DNGWLYISPRLTFPSLQALVDHY 176

RESULT 3
AAU91308
ID AAU91308 standard; Protein; 261 AA.
XX
AC AAU91308;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human protein NOV13.
XX
KW Human; NOVX; gene therapy; cardiomyopathy; atherosclerosis;
KW cell signal processing disorder; metabolic pathway modulation disorder;
KW diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer;
KW uterus cancer; immune response; graft-versus-host disease;
KW acquired immunodeficiency syndrome; AIDS; asthma; Crohn's disease;
KW hypertension; congenital heart defects; multiple sclerosis; inflammation;
KW Albright hereditary osteodystrophy.
XX
OS Homo sapiens.
XX
PN WO200216599-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US26510.
XX
PR 25-AUG-2000; 2000US-228191P.
PR 08-FEB-2001; 2001US-267300P.
PR 20-FEB-2001; 2001US-269961P.
PR 20-MAR-2001; 2001US-277337P.
XX
PA (CURA-) CURAGEN CORP.
PA (CORT-) COR THERAPEUTICS INC.
XX
PI Burgess CE, Conley PB, Grosse WM, Hart M, Kekuda R, Shimkets RA;
PI Spytek KA, Szekeres ES, Tomlinson JE, Topper JN, Yang R;
XX
DR WPI; 2002-280937/32.
DR N-PSDB; ABK61465.
XX
PT New polypeptides for treating or preventing a disorder associated with
PT them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers -
XX
PS Claim 3; Page 98; 263pp; English.
XX
CC The invention relates to an isolated polypeptide (NOVX) a mature
CC form of NOVX, a NOVX variant (differing by no more than 15%), the
CC nucleotide encoding NOVX (or its complement, fragment or variant).
CC NOVX is NOV1-14, 15a, 15b, 16a, and 16b. The NOVX polypeptide, nucleic
CC acid encoding it and antibody against it, are useful for treating or
CC preventing (e.g. by gene therapy) a NOVX-associated disorder in humans,

CC e.g. cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC processing and metabolic pathway modulation, diabetes or cancers. The
CC NOVX polypeptide and nucleic acids are also useful for determining the
CC presence of predisposition to the diseases. The NOVX nucleic acid and
CC polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant NOVX expression or
CC activity, e.g. cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or
CC uterus cancer), immune response, graft-versus-host disease, acquired
CC immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension,
CC congenital heart defects, multiple sclerosis, inflammation or Albright
CC hereditary osteodystrophy and many other diseases listed in the
CC specification. The DNA encoding the protein is useful in gene therapy
CC for treating the conditions. This is also useful in detection assays,
CC chromosome mapping, tissue typing, diagnostic or prognostic assays, or
CC for developing a powerful assay system for functional analysis of
CC various human disorders, as well as in diagnostic applications. The
CC present sequence represents a NOVX protein.
XX
SQ Sequence 261 AA;

Query Match 100.0%; Score 446; DB 23; Length 261;
Best Local Similarity 100.0%; Pred. No. 5.1e-50;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 94 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 153

Qy 61 DNGWLYISPRLTFPSLQALVDHY 83
|||||||||||||||||||||||
Db 154 DNGWLYISPRLTFPSLQALVDHY 176

RESULT 4
AAB42993
ID AAB42993 standard; Protein; 248 AA.
XX
AC AAB42993;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2757 polypeptide sequence SEQ ID NO:5514.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR N-PSDB; AAC77202.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 11; Page 4693-4694; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 248 AA;

Query Match 99.3%; Score 443; DB 21; Length 248;
Best Local Similarity 98.8%; Pred. No. 1.2e-49;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db 81 WLYEGLSREKAEDLLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 140

Qy 61 DNGWLYISPRLTFPSLQALVDHY 83
|||||||||||||||||||||||
Db 141 DNGWLYISPRLTFPSLQALVDHY 163

RESULT 5
AAO15456
ID AAO15456 standard; Protein; 259 AA.
XX
AC AAO15456;
XX
DT 03-OCT-2002 (first entry)
XX
DE Mouse modulator of antigen receptor signalling (MARS) protein.
XX
KW Mouse; gene therapy; modulator of antigen receptor signalling; MARS;
KW tumour suppressor gene; Scr-like adaptor protein; SLAP;
KW myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder;
KW immunosuppression; myeloproliferative disorder; breast cancer.
XX
OS Mus sp.
XX
PN WO200242452-A2.
XX
PD 30-MAY-2002.
XX
PF 26-NOV-2001; 2001WO-CA01662.
XX
PR 27-NOV-2000; 2000CA-2324663.
XX

PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
PI Mcglade JC, Loreto MP;
XX
DR WPI; 2002-566564/60.
DR N-PSDB; AAL44087.
XX
PT New isolated modulator of antigen receptor signaling protein or its
PT fragment, useful for treating malignant disorders such as myeloid
PT malignancies, autoimmune disorders and myeloproliferative disorders -
XX
PS Claim 7; Fig 1A; 110pp; English.
XX
CC The invention comprises the amino acid and coding sequences of modulator
CC of antigen receptor signalling (MARS) proteins. The MARS protein is a
CC putative tumour suppressor gene and exhibits structural and sequence
CC similarity to the Scr-like adaptor protein (SLAP). The MARS DNA and
CC protein sequences of the invention are useful for the treatment of
CC myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune
CC disorders, immunosuppression, myeloproliferative disorders and
CC malignancies related to the de-regulation of tyrosine kinases (e.g.
CC breast cancer). The present amino acid sequence represents a mouse MARS
CC protein.
XX
SQ Sequence 259 AA;

Query Match 92.4%; Score 412; DB 23; Length 259;
Best Local Similarity 94.0%; Pred. No. 1.5e-45;
Matches 78; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
Db 93 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGCYSLSVRLSRPASWDRIRHYRIQRL 152

Qy 61 DNGWLYISPRLTFPSLQALVDHY 83
Db 153 DNGWLYISPRLTFPSLHALVEHY 175

RESULT 6
AAB99332
ID AAB99332 standard; Protein; 505 AA.
XX
AC AAB99332;
XX
DT 23-AUG-2001 (first entry)
XX
DE Human tyrosine kinase Hck protein sequence SEQ ID NO:11.
XX
KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
KW Hck signal transduction; human immunodeficiency virus; HIV infection;
KW anticancer.
XX
OS Homo sapiens.
XX
PN WO200132869-A1.
XX
PD 10-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-JP07500.
XX
PR 29-OCT-1999; 99JP-0309957.
XX
PA (SSSE) SSP CO LTD.
XX
PI Taniyama T, Narita T;
XX
DR WPI; 2001-316440/33.
XX
PT New proteins which bind to human tyrosine kinase Hck for promotion of
PT apoptosis and for the elucidation of the mechanism of Hck signal
PT transduction -
XX
PS Example 1; Page 33-35; 45pp; Japanese.
XX
CC The present invention describes a protein, designated HSB-1, which binds
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
CC encoding the protein and its derivatives; (2) recombinant vectors
CC containing the nucleic acids; and (3) host cells transformed by the
CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds
CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
CC of Hck signal transduction and of the role of Hck in human
CC immunodeficiency virus (HIV) infection. They can be used for the
CC treatment of infections and other diseases with which Hck is associated.
CC They promote the anticancer activity of tumour necrosis factor alpha.
CC The present sequence represents the human tyrosine kinase Hck protein,
CC which is used in an example from the present invention.
XX
SQ Sequence 505 AA;

Query Match 57.0%; Score 254; DB 22; Length 505;
Best Local Similarity 57.8%; Pred. No. 1.9e-24;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
Db 123 WFFKGISRKDAERQLLAPGNMLGSFMIRDSETTKGSYSLSVRDYDPRQGDTVKHYKIRTL 182

Qy 61 DNGWLYISPRLTFPSLQALVDHY 83
Db 183 DNGGFYISPRSTFSTLQELVDHY 205

RESULT 7
AAU31072
ID AAU31072 standard; Protein; 315 AA.
XX
AC AAU31072;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #1563.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX
PS Claim 20; Page 399; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 315 AA;

Query Match 52.2%; Score 233; DB 22; Length 315;
Best Local Similarity 56.6%; Pred. No. 6e-22;
Matches 47; Conservative 12; Mismatches 18; Indels 6; Gaps 1;

```
Qy       1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
           ||:||| |:|||||| ||    |:|:||||:|::| ||||||        ::: |||  |
Db     123 WLFEGLGRDKAEELLQLPDTKVGSFMIRESETKKGFYSLSVR------HRQVKTYRIFRL 176

Qy      61 DNGWLYISPRLTFPSLQALVDHY 83
             | | |||||||||  |: ||:||
Db     177 PNNWYYISPRLTFQCLEDLVNHY 199
```

RESULT 8
AAW31184
ID AAW31184 standard; Protein; 101 AA.
XX
AC AAW31184;
XX
DT 11-MAR-1998 (first entry)
XX
DE Human p56-lck protein SH2 domain.
XX
KW p62; cytoplasmic; T cell; B cell; development; activation; modulation;
KW cellular response; cell proliferation; autoimmune disease; p56-lck;
KW SH2 binding domain.
XX
OS Homo sapiens.
XX
PN WO9722255-A1.
XX
PD 26-JUN-1997.
XX
PF 11-DEC-1996; 96WO-US19944.
XX
PR 19-DEC-1995; 95US-0574959.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Joung I, Shin J, Strominger JL, Vadlamudi RK;
XX
DR WPI; 1997-341351/31.
XX
PT cDNA encoding p62 and p160 and corresponding proteins - used in the
PT treatment of autoimmune disease and for T and B cell proliferation,
PT e.g. for treatment of tumours
XX
PS Disclosure; Fig 5; 175pp; English.
XX
CC This sequence represents the p56-lck SH2 binding domain which is
CC capable of binding the p62 sequences represented in AAW31182 and
CC AAW31183 in a phosphotyrosine (pY) independent manner. Such p62
CC polypeptides with this activity are capable of modulating T or B cell
CC development and/or T or B cell activation e.g. by modulation of Lck
CC activity. They are also capable of modulating degradation of cellular
CC proteins e.g. cell cycle regulatory proteins stimulating expression of
CC cell cycle dependent kinase inhibitors and arresting cell cycle
CC progression at specific boundaries to thereby modulate cell
CC proliferation. As p62 acts to boost B cell response and may be used to
CC treat disorders where this is beneficial, e.g. infections by pathogenic
CC microorganisms, e.g. bacteria, viruses and protozoans. p62 can be used
CC to expand T cell populations for treating infectious diseases or cancer,
CC e.g. the resulting cells may be transduced to render them resistant to
CC HIV infection. Inhibitors of p62 can be used to reduce B or T cell
CC responses and may be used to treat a variety of autoimmune diseases,
CC e.g. diabetes mellitus, arthritis, multiple sclerosis allergic reactions
CC and Crohn's disease.
XX
SQ Sequence 101 AA;

Query Match 51.1%; Score 228; DB 18; Length 101;
Best Local Similarity 54.2%; Pred. No. 6.2e-22;
Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

```
Qy       1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
           | :: |||: ||  || |||  |:||||||::  ||:|||||       : ::||:|  |
Db       1 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 60

Qy      61 DNGWLYISPRLTFPSLQALVDHY 83
             |||  |||||:||| |  || ||
Db      61 DNGGFYISPRITFPGLHELVRHY 83
```

RESULT 9
AAW03982
ID AAW03982 standard; Peptide; 134 AA.
XX
AC AAW03982;
XX
DT 30-APR-1997 (first entry)
XX
DE DET1-DET2-spacer-ek-lck SH2 construct.
XX
KW Polymerase chain reaction; PCR; amplify; primer; chicken; src;
KW SH2 domain; DET1; DET2; erythropoiesis; anaemia; haematopoiesis;
KW antagonist.
XX
OS Synthetic.
XX
PN EP728482-A2.
XX
PD 28-AUG-1996.
XX
PF 07-FEB-1996; 96EP-0200269.
XX
PR 29-DEC-1995; 95US-0581089.
PR 10-FEB-1995; 95US-0386381.
PR 07-MAR-1995; 95US-0400220.
PR 30-JUN-1995; 95US-0497357.
PR 11-OCT-1995; 95US-0540680.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Dunnington DJ;
XX
DR WPI; 1996-386024/39.
XX
PT Use of selective antagonist of haematopoietic acid phosphatase SH2
PT domain - with no significant affinity for other SH2 domains, to
PT increase erythropoiesis and haematopoiesis, esp. for treatment of
PT anaemia
XX
PS Example 3; Page 28-29; 46pp; English.
XX
CC This sequence represents the DET1-DET2-spacer-ek-lck SH2 construct
CC encoded by the sequence amplified by the primers given in AAT37297-98.
CC This protein fragment was used in the isolation of a compound for
CC improving erythropoiesis. The compound may be used for the treatment
CC of anaemia or to enhance haematopoiesis. The isolated compound
CC antagonises the hcp SH2 domain without side effects caused by
CC non-specific inhibition of other SH2 domains.

```
XX
SQ   Sequence   134 AA;

  Query Match             51.1%;  Score 228;  DB 17;  Length 134;
  Best Local Similarity   54.2%;  Pred. No. 9e-22;
  Matches   45;  Conservative   12;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
           | :: |||: ||  || |||  |:||||||::  ||:|||||       : ::||:|  |
Db      31 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 90

Qy      61 DNGWLYISPRLTFPSLQALVDHY 83
           |||  |||||:||| |  || ||
Db      91 DNGGFYISPRITFPGLHELVRHY 113


RESULT 10
AAW02120
ID   AAW02120 standard; Protein; 134 AA.
XX
AC   AAW02120;
XX
DT   28-OCT-1996  (first entry)
XX
DE   DET1-DET2-spacer-ek-lck SH2 construct.
XX
KW   Bone resorption disease; osteoporosis; src SH2 domain antagonist;
KW   src homology 2 domain; lck SH2 domain.
XX
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          2..12
FT                   /label= DET1
FT                   /note= "defined epitope tag from HIV-1 gp120/160"
FT   Region          13..18
FT                   /label= DET2
FT                   /note= "hexahistidine tag"
FT   Region          19..21
FT                   /label= Spacer
FT   Region          22..26
FT                   /label= EK
FT                   /note= "enterokinase cleavage site"
FT   Domain          27..130
FT                   /label= lck-SH2_domain
XX
PN   EP727211-A1.
XX
PD   21-AUG-1996.
XX
PF   07-FEB-1996;   96EP-0200270.
XX
PR   29-DEC-1995;   95US-0580868.
PR   10-FEB-1995;   95US-0386381.
PR   07-MAR-1995;   95US-0400220.
PR   30-JUN-1995;   95US-0497357.
PR   11-OCT-1995;   95US-0541080.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Dunnington DJ;
XX
DR   WPI; 1996-372674/38.
XX
PT   Use of selective src SH2 domain ligand - to prepare medicament for
PT   treating bone resorption disease
XX
PS   Example 11; Page 28-29; 47pp; English.
XX
CC   Construct DET1-DET2-spacer-ek-lck SH2 (AAW02120) was obtd. by
CC   inserting a PCR fragment (see also AAT36190-91) coding for human lck
CC   SH2 domain into a vector contg. a tagged chicken src gene
CC   DET1-DET2-spacer-SH2 (see also AAT36186-87).  The construct can be
CC   expressed in E. coli and used, together with similar constructs (see
CC   also AAW02119-21 and AAW02124-27), in binding assays to determine the
CC   specificity of cpds. to inhibit SH2 domains; cpds. that selectively
CC   inhibit the human src SH2 domain are useful in treating bone
CC   resorption diseases such as osteoporosis.
XX
SQ   Sequence   134 AA;

  Query Match             51.1%;  Score 228;  DB 17;  Length 134;
  Best Local Similarity   54.2%;  Pred. No. 9e-22;
  Matches   45;  Conservative   12;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
           | :: |||: ||  || |||  |:||||||::  ||:|||||       : ::||:|  |
Db      31 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 90

Qy      61 DNGWLYISPRLTFPSLQALVDHY 83
           |||  |||||:||| |  || ||
Db      91 DNGGFYISPRITFPGLHELVRHY 113


RESULT 11
AAW11286
ID   AAW11286 standard; peptide; 134 AA.
XX
AC   AAW11286;
XX
DT   10-NOV-1997  (first entry)
XX
DE   DET1-DET2-spacer-ek-lck SH2 fusion protein.
XX
KW   HIV-1; gp120; defined epitope tag; DET1; envelope protein; human; Stat 6;
KW   signal transduction and activation of transcription; Src homology 2;
KW   signalling molecule; protein tyrosine kinase; oncogenic protein; hcp SH2;
KW   Grb2 SH2; allergic reaction; erythrocyte production; inhibitor; p85 SH2;
KW   asthma; allergic rhinitis; atopic dermatitis; IgE receptor; SH-PTP2 SH2;
KW   interleukin-4; IL-4; SH2 domain; Stat5 SH2; src SH2; lck SH2; fyn SH2;
KW   IL-13; therapy; fusion protein.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         2..12
FT                   /note= "defined epitope tag 1 (DET1)"
FT   Peptide         13..18
FT                   /note= "defined epitope tag 2 (DET2)"
FT   Peptide         19..21
FT                   /note= "spacer"
FT   Peptide         22..26
FT                   /note= "enteroprotein kinase recognition sequence"
FT   Peptide         27..134
FT                   /note= "human lck SH2 domain"
XX
PN   WO9702023-A1.
XX
PD   23-JAN-1997.
XX
PF   28-JUN-1996;   96WO-US11074.
XX
PR   08-FEB-1996;   96US-0598716.
PR   30-JUN-1995;   95US-0497357.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Dunnington DJ;
XX
DR   WPI; 1997-108735/10.
XX
PT   Treating allergies with specific inhibitor of human Stat 6 SH2
PT   domain - having very low binding affinity to panel of other SH2
PT   domains so free of side effects, specifically for asthma and
PT   allergic rhinitis
```

```
XX
PS   Example 11; Page 51-52; 88pp; English.
XX
CC   AAW11285-W11288 represent fusion proteins containing Src homology 2
CC   (SH2) domains. These sequences are used to identify a compound that
CC   targets the human Stat (signal transduction and activation of
CC   transcription) 6 SH2 domain. The identified compounds have a binding
CC   affinity for Stat 6 over 50 (preferably 100) times higher than its
CC   affinity for the human Stat5 SH2 domain. The compound has an affinity for
CC   hcp SH2, SH-PTP2 SH2, p85 SH2, Grb2 SH2, src SH2, lck SH2 or fyn SH2 of
CC   more than 50 (preferably 100) times lower than its affinity for Stat 6
CC   SH2. SH2 domains are conserved non-catalytic sequences found in a variety
CC   of signalling molecules, such as non-receptor protein tyrosine kinases,
CC   and in oncogenic proteins. The compounds identified using the fusion
CC   proteins are used as the administered compound in the method of the
CC   invention for treating allergic reactions. Administration of the compound
CC   avoids the side effects (e.g. reduced erythrocyte production) associated
CC   with non-selective inhibition of SH2 domains. Selective compounds can be
CC   identified in competitive binding assays using only a small subset (the
CC   domains specified above) of SH2 domains rather than all 60 known
CC   domains. The method can be used for the treatment of asthma and allergic
CC   rhinitis, but can also be used to treat atopic dermatitis. Inhibition of
CC   the human Stat 6 SH2 domain blocks up-regulation of the IgE receptor
CC   mediated by interleukin-4 (IL-4) or IL-13.
XX
SQ   Sequence   134 AA;

  Query Match             51.1%;  Score 228;  DB 18;  Length 134;
  Best Local Similarity   54.2%;  Pred. No. 9e-22;
  Matches   45;  Conservative   12;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
           | :: |||: ||  || |||  |:||||||::  ||:|||||       : ::||:|  |
Db      31 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 90

Qy      61 DNGWLYISPRLTFPSLQALVDHY 83
           |||  |||||:||| |  || ||
Db      91 DNGGPYISPRITFPGLHELVRHY 113


RESULT 12
AAW19624
ID   AAW19624 standard; Protein; 134 AA.
XX
AC   AAW19624;
XX
DT   27-OCT-1997  (first entry)
XX
DE   Human lck SH2 domain fusion protein.
XX
KW   Stat 5; Signal Transduction and Activation of Transcription;
KW   Src homology domain; SH2; erythropoiesis enhancing; anaemia;
KW   fusion protein; ek; enterokinase; epitope; antibody production;
KW   detection; HIV; human immunodeficiency virus type 1; gp120;
KW   glycoprotein 120; selective.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         2..12
FT                   /note= "defined epitope tag 1 from HIV gp120"
FT   Peptide         13..18
FT                   /note= "hexahistidine sequence tag"
FT   Region          19..21
FT                   /label= spacer
FT   Cleavage-site   22..26
FT                   /note= "enterokinase protease recognition site"
FT   Peptide         27..134
FT                   /note= "lck SH2"
XX
PN   WO9702024-A1.
XX
PD   23-JAN-1997.
XX
PF   28-JUN-1996;   96WO-US11158.
XX
PR   08-FEB-1996;   96US-0598715.
PR   30-JUN-1995;   95US-0497357.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Dunnington DJ;
XX
DR   WPI; 1997-108736/10.
XX
PT   Enhancing erythropoiesis with specific activator of human Stat 5 SH2
PT   domain - has very low binding affinity to other SH2 domains so free
PT   of side effects, particularly for treating anaemia
XX
PS   Example 11; Page 54-55; 91pp; English.
XX
CC   AAW19624 is a fusion protein of formula DET1-DET2-Sp-ek-SH2, where
CC   DET1 is a defined epitope tag from HIV-1 gp120, DET2 is a hexahistidine
CC   sequence tag (binds to nickel-containing resins, used for purification),
CC   Sp is a spacer, ek is an enterokinase protease recognition site and SH2
CC   is the human lck SH2 domain. DET1 is included so that antibodies
CC   against the epitope can be used to detect the recombinant expression
CC   of the fusion protein and hence the SH2 domain. The fusion proteins
CC   are used for identifying compounds that bind the SH2 domain causing
CC   its activation.
XX
SQ   Sequence   134 AA;

  Query Match             51.1%;  Score 228;  DB 18;  Length 134;
  Best Local Similarity   54.2%;  Pred. No. 9e-22;
  Matches   45;  Conservative   12;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
           | :: |||: ||  || |||  |:||||||::  ||:|||||       : ::||:|  |
Db      31 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 90

Qy      61 DNGWLYISPRLTFPSLQALVDHY 83
           |||  |||||:||| |  || ||
Db      91 DNGGFYISPRITFPGLHELVRHY 113


RESULT 13
AAW14788
ID   AAW14788 standard; Protein; 224 AA.
XX
AC   AAW14788;
XX
DT   20-JUN-1997  (first entry)
XX
DE   FKBP-LCK:SH2 fusion protein.
XX
KW   FKBP-LCK:SH2; FK506 binding protein; SH2 domain; Src homology 2;
KW   fusion protein; high throughput assay; signal transduction; ligand;
KW   microscintillation.
XX
OS   Homo sapiens.
XX
PN   WO9710253-A1.
XX
PD   20-MAR-1997.
XX
PF   11-SEP-1996;   96WO-US14567.
XX
PR   12-MAR-1996;   96GB-0005210.
PR   15-SEP-1995;   95US-0003819.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Marcy A,  Salowe SP,  Wisniewski D;
XX
DR   WPI; 1997-202171/18.
```

DR N-PSDB; AAT63421.
XX
PT Screening compounds for binding to fusion proteins with defined
PT ligands - allows high capacity assays and identification of
PT (ant)agonists or inhibitors for drug development
XX
PS Claim 32; Page 21-22; 36pp; English.
XX
CC Novel fusion proteins FKBP-ZAP:SH2, FKBP-SYK:SH2 and FKBP-LCK:SH2
CC (AAW14786-88) comprise FK506 binding protein (FKBP) linked via a
CC peptide linker to a target protein composed of a multiple signal
CC transduction domain, i.e. ZAP:SH2, SYK:SH2 or LCK:SH2. They can
CC be produced in transformed host cells, esp. E. coli, using
CC expression vectors with fusion protein DNA sequences (AAT63419-21).
CC The fusion proteins are used in novel methods utilising
CC microscintillation plate technology for the functional assay of
CC ligand binding to a signal transduction domain (i.e. SH2). The
CC method is readily adaptable to robotic automation for high
CC capacity screening for agonists, antagonists and/or inhibitors
CC for use in drug development.
XX
SQ Sequence 224 AA;

Query Match 51.1%; Score 228; DB 18; Length 224;
Best Local Similarity 54.2%; Pred. No. 1.7e-21;
Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
Db 125 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 184

Qy 61 DNGWLYISPRLTFPSLQALVDHY 83
Db 185 DNGGFYISPRITFPGLHELVRHY 207

RESULT 14
AAW96823
ID AAW96823 standard; Protein; 224 AA.
XX
AC AAW96823;
XX
DT 21-APR-1999 (first entry)
XX
DE A fusion protein of FKBP-Lck.
XX
KW Fusion protein; FK506 binding protein; FKBP; SH2 domain; human Lck;
KW screening; protein binding; ligand-protein interaction;
KW protein-protein interaction; protease inhibitor.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9841866-A1.
XX
PD 24-SEP-1998.
XX
PF 10-MAR-1998; 98WO-US04610.
XX
PR 14-MAR-1997; 97US-0040795.
XX
PA (MERI) MERCK & CO INC.
XX
PI Hermes JD, Salowe SP, Sinclair PJ;
XX
DR WPI; 1999-070061/06.
DR N-PSDB; AAX15151.
XX
PT High throughput screening assay - for screening compounds capable of
PT binding to a fusion protein consisting of, e.g., a target protein
PT and an FK506-binding protein.
XX
PS Disclosure; Page 26; 42pp; English.
XX
CC The present sequence represents a fusion protein comprising FK506 binding
CC protein (FKBP) and the SH2 domain of human Lck. The protein is used
CC to exemplify the method of the invention. The specification describes a
CC method for screening for compounds capable of binding to a fusion
CC protein. The method comprises mixing a test compound, a biotinylated
CC ligand, the fusion protein, a donor-labelled ligand and acceptor-labeled
CC streptavidin, incubating the mixture, measuring the time-resolved
CC fluorescence attributable to the binding of the biotinylated ligand
CC to the fusion protein in the presence of the test compound and
CC determining the binding of the biotinylated ligand to the fusion protein
CC in the presence of the test compound relative to a control assay run in
CC the absence of the test compound. The methods may be used to determine
CC if compounds are capable of binding to a protein or are capable of
CC blocking ligand-protein or protein-protein interactions. They may be
CC used to identify compounds which are protease inhibitors.
XX
SQ Sequence 224 AA;

Query Match 51.1%; Score 228; DB 20; Length 224;
Best Local Similarity 54.2%; Pred. No. 1.7e-21;
Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
Db 125 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 184

Qy 61 DNGWLYISPRLTFPSLQALVDHY 83
Db 185 DNGGFYISPRITFPGLHELVRHY 207

RESULT 15
AAB37700
ID AAB37700 standard; protein; 508 AA.
XX
AC AAB37700;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human lymphocyte kinase.
XX
KW Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.
XX
OS Homo sapiens.
XX
PN WO200070030-A1.
XX
PD 23-NOV-2000.
XX
PF 19-MAY-2000; 2000WO-US13881.
XX
PR 19-MAY-1999; 99US-0134965.
XX
PA (KINE-) KINETIX PHARM INC.
XX
PI Zhu X;
XX
DR WPI; 2000-687708/67.
XX
PT Crystal of a protein-ligand complex for identifying kinase inhibitors,
PT comprises a truncated lymphocyte kinase and a ligand, and diffracts
PT X-rays to determine atomic coordinates at a resolution greater than 5
PT angstroms -
XX
PS Claim 1; Page 434-5; 438pp; English.
XX
CC The present invention relates to a crystal of a protein-ligand complex
CC comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal
CC diffracts X-rays so that the atomic coordinates of the protein-ligand
CC complex can be determined to a resolution of greater than 5.0 Angstroms.
CC The truncated lck used in the present invention comprises the globular
CC core of the corresponding full-length lck. The present sequence is the

CC full-length human lck protein. The crystal of the present invention may
CC be used to identify kinase inhibitors in screening assays, in drug
CC screening and drug design processes, to design, select or test inhibitors
CC of kinase enzymes, where the inhibitors are used as therapeutics for the
CC treatment and modulation of diseases, disease symptoms or the effect of
CC other physiological events mediated by kinases, having one or more kinase
CC enzymes involved in their pathology.
XX
SQ Sequence 508 AA;

Query Match 51.1%; Score 228; DB 21; Length 508;
Best Local Similarity 54.2%; Pred. No. 5e-21;
Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

```
Qy       1 WLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 60
           | :: |||: ||  || |||  |:||||||::  ||:|||||      : ::||:|  |
Db     126 WFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNL 185

Qy      61 DNGWLYISPRLTFPSLQALVDHY 83
           |||  |||||:||| |  || ||
Db     186 DNGGFYISPRITFPGLHELVRHY 208
```

Search completed: March 24, 2003, 15:48:37
Job time : 18.6061 secs